

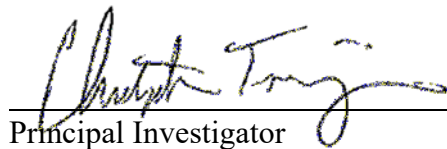
USDA-ARS
U.S. Wheat and Barley Scab Initiative
FY17 Preliminary Final Performance Report
Due date: July 31, 2018

Cover Page

Principle Investigator (PI):	Christopher Toomajian
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Fiscal Year:	2017
USDA-ARS Agreement ID:	59-0200-6-002
USDA-ARS Agreement Title:	Finding Fusarium graminearum Genes to Target using Population Genomics.
FY17 USDA-ARS Award Amount:	\$ 47,247
Recipient Organization:	Kansas State University 10 Anderson Hall Manhattan, KS 66506
DUNS Number:	929773554
EIN:	48-0771751
Recipient Identifying Number or Account Number:	AR9855, GAPP603891
Project/Grant Reporting Period:	4/21/17 - 4/20/18
Reporting Period End Date:	4/20/2018

USWBSI Individual Project(s)

USWBSI Research Category*	Project Title	ARS Award Amount
PBG	Population Genomics to Identify Fusarium graminearum Genes to Target.	\$ 47,247
	FY17 Total ARS Award Amount	\$ 47,247


Principal Investigator

July 31, 2018

Date

* MGMT – FHB Management
FST – Food Safety & Toxicology
GDER – Gene Discovery & Engineering Resistance
PBG – Pathogen Biology & Genetics
EC-HQ – Executive Committee-Headquarters
BAR-CP – Barley Coordinated Project
DUR-CP – Durum Coordinated Project
HWW-CP – Hard Winter Wheat Coordinated Project
VDHR – Variety Development & Uniform Nurseries – Sub categories are below:
SPR – Spring Wheat Region
NWW – Northern Soft Winter Wheat Region
SWW – Southern Soft Red Winter Wheat Region

Project 1: *Population Genomics to Identify Fusarium graminearum Genes to Target.*

1. What are the major goals and objectives of the project?

The goal of our project is to identify genes harboring functional variation that contributes to variation in important pathogen traits (pathogenicity, mycotoxin production, measures of fitness) within *F. graminearum* (*Fg*) populations to provide targets for pathogen control.

Project objectives:

- Phenotype approximately 150 *Fg* isolates from the over 500 isolates genotyped in our FY14-15 project, our subset composed of isolates chosen to represent the full genetic diversity of the previously genotyped isolates from the US.
- Perform genome-wide association studies (GWAS) of the above traits, taking into account population structure. Polymorphisms associated with pathogen traits will be compared to the results of the scans for natural selection from our FY14-15 project as well as aggressiveness or mycotoxin production QTL identified by other groups through biparental mapping strategies.

2. What was accomplished under these goals? *Address items 1-4) below for each goal or objective.*

A number of the plans for the reporting period had to be adjusted due to unanticipated events. In addition to being on paternity leave for parts of the beginning of this reporting period, my PhD student Wei Yue who had served as project personnel graduated during the reporting period, and I was not able to recruit a suitable replacement to complete the work immediately. As such, I requested and was granted a no-cost twelve month time extension for this project in order that it may be successfully completed, without changing the scope of the work or cost of the project. Despite these setbacks, we were still able to accomplish related activities for the project during this reporting period.

- 1) Major activities: A number of the major activities for this objective were postponed as explained above. Only preliminary laboratory experiments on isolate growth rates in culture have been performed at this stage of the project.
- 2) **Specific objective 1:** This objective included measuring two classes of traits – virulence traits of the *Fg* isolates on wheat as well as saprophytic traits and measures of DON accumulation of isolates in the laboratory.
- 3) Significant results: At this stage we have no significant results to report on additional isolate phenotyping.
- 4) Key outcomes or other achievements: No key outcomes achieved yet for this objective.

- 1) Major activities: So far our activities related to this objective include re-analyzing population structure in our full set of 570 *Fusarium* isolates using newly available software that can provide greater resolution of subpopulation membership of each isolate and the evolutionary relationships between the subpopulations. Additionally, we performed a genome scan using our SNP genotypes from our full sample of 570 isolates for evidence of recent selective sweeps in this genetic variation data. As greenhouse trait collection had been largely postponed, we have no GWAS-specific activities to report for this objective outside of the preliminary GWAS that we had already performed before the current reporting period.
- 2) **Specific objective 2:** This objective included performing genome-wide association mapping of traits measured in objective 1 to look for SNPs identified in our previous project associated with these traits.
- 3) Significant results: Our re-analysis of population structure in our full sample of 570 *Fusarium* isolates has provided a complete and accurate picture of the relationship between these isolates and reveals broader patterns, especially regarding their geographical origin and trichothecene (TRI) genotypes. Our sample composition allowed us to demonstrate the close relationship between 15-ADON isolates collected from Uruguay with many US 3-ADON isolates, as well as indicated how different subpopulations from Louisiana were related to isolates from the Upper Midwest and New York state. The genome scan for selective sweeps we have performed using patterns of allele frequency from our SNPs is only preliminary, as we have not yet made comparisons to closely related species to infer which alleles are ancestral and which are the derived alleles that result from more recent mutation events. On a related dataset, we have recently performed species comparisons to infer ancestral and derived states, and with the publicly available *Fusarium* genomes and the analysis pipeline we have in place, it should be quick and easy to infer ancestral and derived states for our SNPs from this project, leading to a more powerful scan. Nevertheless, the current scan already indicates the chromosomal regions most likely to be affected by recent sweeps that highlight potential genes related to pathogen fitness that could serve as targets for control of the pathogen.
- 4) Key outcomes or other achievements: Due to the postponement of several major activities from this objective, we have not yet achieved major key outcomes for this objective.

3. What opportunities for training and professional development has the project provided?

During the current reporting period, the project has provided training for Ph.D. student Wei Yue, support personnel for this project, and visiting Ph.D. student and collaborator Vero Fumero. Both received training on modern genotyping technologies relevant for *Fusarium* as well as bioinformatics and population genetic analytical techniques. PI Toomajian used data from USWBSI projects in teaching his graduate Population Genetics class to 14 students in the spring of 2017. Additionally, both PIs provided instruction and lectures to 52 participants

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in the June 2017 International Fusarium Laboratory Workshop at Kansas State University in Manhattan, KS. Finally, co-PI Leslie provided professional development opportunities in the form of Scientific Writing Courses taught at: University of Vienna (BOKU), Tulln, Austria; Institute for the Science of Food Production, Bari, Italy; and University of Viçosa, Viçosa, Brazil.

4. How have the results been disseminated to communities of interest?

During the current period, results from this project have been disseminated through participation at the following conferences: attendance with a poster presentation at the 2017 Scab Forum by PI Toomajian and attendance with presentations at the September 2017 1st MYCOKEY International Conference in Ghent, Belgium. Co-PI Leslie also gave two radio interviews and both PIs participated in Kansas State University's annual open house for the purpose of outreach to enhance public understanding of plant pathology and increase interest in careers in this field.

Training of Next Generation Scientists

Instructions: Please answer the following questions as it pertains to the FY17 award period. The term “support” below includes any level of benefit to the student, ranging from full stipend plus tuition to the situation where the student’s stipend was paid from other funds, but who learned how to rate scab in a misted nursery paid for by the USWBSI, and anything in between.

1. **Did any graduate students in your research program supported by funding from your USWBSI grant earn their MS degree during the FY17 award period?**
No
If yes, how many?

2. **Did any graduate students in your research program supported by funding from your USWBSI grant earn their Ph.D. degree during the FY17 award period?**
Yes
If yes, how many?
2

3. **Have any post docs who worked for you during the FY17 award period and were supported by funding from your USWBSI grant taken faculty positions with universities?**
No
If yes, how many?

4. **Have any post docs who worked for you during the FY17 award period and were supported by funding from your USWBSI grant gone on to take positions with private ag-related companies or federal agencies?**
No
If yes, how many?

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Release of Germplasm/Cultivars

Instructions: In the table below, list all germplasm and/or cultivars released with full or partial support through the USWBSI during the FY17 award period. All columns must be completed for each listed germplasm/cultivar. Use the key below the table for Grain Class abbreviations. *Leave blank if you have nothing to report or if your grant did NOT include any VDHR-related projects.*

Name of Germplasm/Cultivar	Grain Class	FHB Resistance (S, MS, MR, R, where R represents your most resistant check)	FHB Rating (0-9)	Year Released

Add rows if needed.

NOTE: List the associated release notice or publication under the appropriate sub-section in the ‘Publications’ section of the FPR.

Abbreviations for Grain Classes

- Barley - BAR
- Durum - DUR
- Hard Red Winter - HRW
- Hard White Winter - HWW
- Hard Red Spring - HRS
- Soft Red Winter - SRW
- Soft White Winter - SWW

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Publications, Conference Papers, and Presentations

Instructions: Refer to the FY17-FPR_Instructions for detailed instructions for listing publications/presentations about your work that resulted from all of the projects included in the FY17 grant. Only include citations for publications submitted or presentations given during your award period (4/21/17 - 4/20/18). If you did not have any publications or presentations, state 'Nothing to Report' directly above the Journal publications section.

NOTE: Directly below each reference/citation, you must indicate the Status (i.e. published, submitted, etc.) and whether acknowledgement of Federal support was indicated in publication/presentation.

Journal publications.

Minnaar-Ontong, A., L. Herselman, W.-M. Kriel and **J.F. Leslie**. 2017. Morphological characterization and trichothecene genotype analysis of a *Fusarium* Head Blight population in South Africa. *Eur J Plant Pathol* 148: 261-269.

Status: Published

Acknowledgement of Federal Support: Indirectly, through the inclusion of Kansas Agricultural Experiment Station manuscript number.

Fumero, M.V., A. Villani, M. Haidukowski, M. T. Cimmarusti, **J. F. Leslie**, **C. Toomajian**, S. Chulze and A. Moretti. 2017. Differences in the beauvericin gene cluster and toxin production in *Fusarium subglutinans* and *Fusarium temperatum*. In: *Proceedings of the 1st Mycokey Conference (Ghent, Belgium)*, p. 165.

Status: Abstract published and poster presented

Acknowledgement of Federal Support: No, publication resulted from other funding source

Perrone, G., J. C. Frisvad, R. A. Samson, **J. F. Leslie**, C. Waalwijk and A. F. Logrieco. 2017. Good practices for preserving biodiversity of mycotoxigenic fungi. In: *Proceedings of the 1st Mycokey Conference (Ghent, Belgium)*, p. 195.

Status: Abstract published and poster presented

Acknowledgement of Federal Support: No, publication resulted from other funding source

Toomajian, C., W. Yue, and J. F. Leslie. 2017. Updating population structure and genetic differentiation of *Fusarium graminearum* populations from three major US regions using genotyping-by-sequencing. In: S. Canty, B. Wiermer and D. Van Sanford (Eds.), *Proceedings of the 2017 National Fusarium Head Blight Forum*. (p. 72) East Lansing, MI/Lexington, KY: U.S. Wheat & Barley Scab Initiative.

Status: Abstract published and poster presented

Acknowledgement of Federal Support: YES (poster), YES (abstract)

Leslie, J. F., V. Lattanzio, K. Audenaert, P. Battilani, J. Cary, S. N. Chulze, S. DeSaeger, A. Gerardino, P. Karlovsky, Y.-C. Liao, C. M. Maragos, G. Meca, A. Medina, A. Moretti, G.

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Munkvold, G. Mule, P. Njobeh, I. Pecorelli, G. Perrone, A. Pietri, J. M. Palazzini, R. H. Proctor, E. S. Rahayu, M. L. Ramirez, R. Samson, J. Stroka, M. Sulyok, M. Sumarah, C. Waalwijk, Q. Zhang, H. Zhang, and A. F. Logrieco. 2018. MycoKey round table discussions of future directions in research on chemical detection methods, genetics and biodiversity of mycotoxins. *Toxins* 10: 109.

Status: Published

Acknowledgement of Federal Support: Indirectly, through the inclusion of Kansas Agricultural Experiment Station manuscript number

Logrieco, A. F., J. D. Miller, M. Eskola, R. Krska, A. Ayalew, R. Bandyopadhyay, P. Battilani, D. Bhatnagar, S. Chulze, S. DeSaeger, P. W. Li, G. Perrone, A. Poapolathep, E. S. Rahayu, G. S. Shephard, F. Stepman, H. Zhang, and **J. F. Leslie**. 2018. The Mycotox Charter: Increasing awareness of, and concerted action for, minimizing mycotoxin exposure worldwide. *Toxins* 10: 149.

Status: Published

Acknowledgement of Federal Support: Indirectly, through the inclusion of Kansas Agricultural Experiment Station manuscript number

Books or other non-periodical, one-time publications.

Yue, W. (2017). *Characterization of genetic variation in secondary metabolites in Fusarium* (Doctoral dissertation). Retrieved from K-Rex K-State Research Exchange (<http://hdl.handle.net/2097/36261>).

Status: Published

Acknowledgement of Federal Support: No

Other publications, conference papers and presentations.

Conference Presentations:

Fumero, M. V., **C. Toomajian**, M. Sulyok, **J. F. Leslie**, and S. N. Chulze. 2017. Fusaric acid gene cluster in *Fusarium temperatum* and *Fusarium subglutinans* and its production under different culture conditions. IX Congreso Latinoamericano de Micología, Lima, Peru, August.

Status: Abstract published and poster presented

Acknowledgement of Federal Support: No, publication resulted from other funding source

Leslie, J. F. and A. F. Logrieco. 2017. Nominal groups for managing discussions and priority setting of issues in mycotoxicology. MycoKey Conference (Ghent, Belgium).

Status: Published

Acknowledgement of Federal Support: No

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Other Presentations:

***Fusarium* Laboratory Workshop, June 2017, Kansas State University, Manhattan KS**

52 participants

John F. Leslie: Workshop organizer and instructor - presented 3 lectures

Christopher Toomajian: Instructor - presented 1 lecture

Status: Lectures presented and slides distributed to workshop participants

Acknowledgement of Federal Support: Resulted from other funding source

Leslie, J. F. 2018. Kansas State University and the PBCRC. Plant Biosecurity Science Exchange
(Melbourne, Australia).

Status: Presentation given

Acknowledgement of Federal Support: No, publication resulted from other funding source.

Leslie, J. F. 2018. Mycotoxin contamination of wheat, raisins and dried fruit in Afghanistan.

School of Natural Sciences, University of Southern Queensland, Toowoomba.

Status: Presentation given

Acknowledgement of Federal Support: YES